



1632

#16

## RAW SEQUENCE LISTING

DATE: 02/19/2002

PATENT APPLICATION: US/09/903,327A

TIME: 15:53:09

Input Set : A:\Pto.amc

Output Set: N:\CRF3\02192002\I903327A.raw

ENTERED

3 <110> APPLICANT: Nemerow, Glen R.  
 4 Li, Erguang  
 6 <120> TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR  
 TARGETED

7 GENE  
 8 DELIVERY  
 10 <130> FILE REFERENCE: 22908-1228  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/903,327A

RECEIVED

FEB 22 2002

TECH CENTER 1600/2900

13 <141> CURRENT FILING DATE: 2001-07-10  
 15 <150> PRIOR APPLICATION NUMBER: 09/613,017  
 16 <151> PRIOR FILING DATE: 2000-07-10  
 18 <160> NUMBER OF SEQ ID NOS: 33  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1516  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Mouse  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (28)...(1395)  
 30 <223> OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody  
 32 <400> SEQUENCE: 1  
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 34 Met Gly Trp Ser Trp Ile Phe Leu Phe  
 35 1 5  
 37 ctc ctg tca gga act gca ggc gtc cac tct gag gtc cag ctt cag cag 102  
 38 Leu Leu Ser Gly Thr Ala Gly Val His Ser Glu Val Gln Leu Gln Gln  
 39 10 15 20 25  
 41 tca gga cct gag ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc 150  
 42 Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys  
 43 30 35 40  
 45 aag gct tct gga tac aca ttc act gac tac aac atg cac tgg gtg aag 198  
 46 Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met His Trp Val Lys  
 47 45 50 55  
 49 cag agc cat gga aag agc ctt gag tgg att gga tat att tat cct tac 246  
 50 Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr  
 51 60 65 70  
 53 aaa ggt ggt act ggc tac aac cag aag ttc aag agc aag gcc aca ttg 294  
 54 Lys Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Ala Thr Leu  
 55 75 80 85  
 57 aca aca gac agt tcc tcc aac aca gcc tac atg gag ctc cgc agc ctg 342  
 58 Thr Thr Asp Ser Ser Ser Asn Thr Ala Tyr Met Glu Leu Arg Ser Leu  
 59 90 95 100 105  
 61 aca tct gat gcc tct gca gtc tat tac tgt gca aga ggg att gct tac 390

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62	Thr	Ser	Asp	Ala	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Ile	Ala	Tyr	
63					110					115				120			
65	tgg	ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	gcc	aaa	acg	aca	ccc	438
66	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Lys	Thr	Thr	Pro	
67				125					130					135			
69	cca	tct	gtc	tat	cca	ctg	gcc	cct	gga	tct	gct	gcc	caa	act	aac	tcc	486
70	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	
71				140					145					150			
73	atg	gtg	acc	ctg	gga	tgc	ctg	gtc	aag	ggc	tat	ttc	cct	gag	cca	gtg	534
74	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	
75				155					160					165			
77	aca	gtg	acc	tgg	aac	tct	gga	tcc	ctg	tcc	agc	ggt	gtg	cac	acc	ttc	582
78	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	
79	170					175						180				185	
81	cca	gct	gtc	ctg	cag	tct	gac	ctc	tac	act	ctg	agc	agc	tca	gtg	act	630
82	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	
83					190						195				200		
85	gtc	ccc	tcc	agc	acc	tgg	ccc	agc	gag	acc	gtc	acc	tgc	aac	gtt	gcc	678
86	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	
87					205					210					215		
89	cac	ccg	gcc	agc	agc	acc	aag	gtg	gac	aag	aaa	att	gtg	ccc	agg	gat	726
90	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	
91				220					225					230			
93	tgt	ggt	tgt	aag	cct	tgc	ata	tgt	aca	gtc	cca	gaa	gta	tca	tct	gtc	774
94	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	
95				235					240					245			
97	ttc	atc	ttc	ccc	cca	aag	ccc	aag	gat	gtg	ctc	acc	att	act	ctg	act	822
98	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	
99	250					255					260					265	
101	cct	aag	gtc	acg	tgt	gtt	gtg	gta	gac	atc	agc	aag	gat	gat	ccc	gag	870
102	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	
103					270						275				280		
105	gtc	cag	ttc	agc	tgg	ttt	gta	gat	gat	gtg	gag	gtg	cac	aca	gct	cag	918
106	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	
107					285					290					295		
109	acg	caa	ccc	cgg	gag	gag	cag	ttc	aac	agc	act	ttc	cgc	tca	gtc	agt	966
110	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	
111				300					305					310			
113	gaa	ctt	ccc	atc	atg	cac	cag	gac	tgg	ctc	aat	ggc	aag	gag	ttc	aaa	1014
114	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	
115				315				320					325				
117	tgc	agg	gtc	aac	agt	gca	gct	ttc	cct	gcc	ccc	atc	gag	aaa	acc	atc	1062
118	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	
119	330					335					340				345		
121	tcc	aaa	acc	aaa	ggc	aga	ccg	aag	gct	cca	cag	gtg	tac	acc	att	cca	1110
122	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	
123					350						355				360		
125	cct	ccc	aag	gag	cag	atg	gcc	aag	gat	aaa	gtc	agt	ctg	acc	tgc	atg	1158
126	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	Met	

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127          365          370          375
129 ata aca gac ttc ttc cct gaa gac att act gtg gag tgg cag tgg aat      1206
130 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
131          380          385          390
133 ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg gac aca      1254
134 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
135          395          400          405
137 gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc aac      1302
138 Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
139 410          415          420          425
141 tgg gag gca gga aat act ttc atc tgc tct gtg tta cat gag ggc ctg      1350
142 Trp Glu Ala Gly Asn Thr Phe Ile Cys Ser Val Leu His Glu Gly Leu
143          430          435          440
145 cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt aaa      1395
146 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
147          445          450          455
149 tgatcccagt gtccttggag ccctctggtc ctacaggact ctgtcaccta cctccacccc      1455
150 tccctgtata aataaagcac cttagcactgc cttgggaccc tgcaataaaaa aaaaaaaaaa      1515
151 a      1516
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 456
155 <212> TYPE: PRT
156 <213> ORGANISM: Mouse
158 <220> FEATURE:
159 <221> NAME/KEY: PEPTIDE
160 <222> LOCATION: (0)...(0)
161 <223> OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
163 <400> SEQUENCE: 2
164 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
165 1          5          10          15
166 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
167          20          25          30
168 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
169          35          40          45
170 Thr Asp Tyr Asn Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
171          50          55          60
172 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Lys Gly Gly Thr Gly Tyr Asn
173 65          70          75          80
174 Gln Lys Phe Lys Ser Lys Ala Thr Leu Thr Thr Asp Ser Ser Ser Asn
175          85          90          95
176 Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Asp Ala Ser Ala Val
177          100          105          110
178 Tyr Tyr Cys Ala Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val
179          115          120          125
180 Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala
181          130          135          140
182 Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu
183 145          150          155          160
184 Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly

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185          165          170          175
186 Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp
187          180          185          190
188 Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
189          195          200          205
190 Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys
191          210          215          220
192 Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile
193 225          230          235          240
194 Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro
195          245          250          255
196 Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val
197          260          265          270
198 Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val
199          275          280          285
200 Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
201          290          295          300
202 Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
203 305          310          315          320
204 Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
205          325          330          335
206 Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
207          340          345          350
208 Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
209          355          360          365
210 Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
211          370          375          380
212 Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
213 385          390          395          400
214 Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
215          405          410          415
216 Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
217          420          425          430
218 Ile Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
219          435          440          445
220 Ser Leu Ser His Ser Pro Gly Lys
221          450          455
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 831
225 <212> TYPE: DNA
226 <213> ORGANISM: Mouse
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (13)...(726)
231 <223> OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
233 <400> SEQUENCE: 3
234 aagcttaccg cc atg gag aca gac aca atc ctg cta tgg gtg ctg ctg ctc      51
235          Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu
236          1          5          10

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238 tgg gtt cca ggc tcc act ggt gac att gtg ctg acc caa tct cca gct      99
239 Trp Val Pro Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala
240      15                20                25
242 tct ttg gct gtg tct cta ggg cag agg gcc acc atc tcc tgc aag gcc      147
243 Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala
244      30                35                40                45
246 agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac caa      195
247 Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln
248                50                55                60
250 cag aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc aat      243
251 Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn
252                65                70                75
254 tta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg aca      291
255 Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr
256                80                85                90
258 gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca acc      339
259 Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr
260                95                100                105
262 tat tac tgt cag caa act aat gag gat ccg tgg acg ttc ggt gga ggc      387
263 Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Trp Thr Phe Gly Gly Gly
264      110                115                120                125
266 acc aag ctg gaa atc aaa cgg gct gat gct gca cca act gta tcc atc      435
267 Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile
268                130                135                140
270 ttc cca cca tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg      483
271 Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val
272                145                150                155
274 tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag      531
275 Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys
276                160                165                170
278 att gat ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act gat      579
279 Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp
280                175                180                185
282 cag gac agc aaa gac agc acc tac agc atg agc acc ctc acg ttg      627
283 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu
284      190                195                200                205
286 acc aag gac gag tat gaa cga cat aac agc tat acc tgt gag gcc act      675
287 Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr
288                210                215                220
290 cac aag aca tca act tca ccc att gtc aag agc ttc aac agg aat gag      723
291 His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu
292                225                230                235
294 tgt tagagacaaa ggtcctgaga cgccaccacc agctccccag ctccatccta      776
295 Cys
298 tcttcccttc taaggctcttg gaggccttcc cgagcggttaa agggcggaatt ccagc      831
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 238
302 <212> TYPE: PRT
303 <213> ORGANISM: Mouse

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\02192002\I903327A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:350 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION: (0)...  
(1314)